

SEQ.ID.NO.:1 Sequence of the Codon-Optimized HPV16L1

ATGAGCCTGTGGCTGCCAGCGAGGCCACCGTGTACCTGCCTCCGTGCCGTGAGCAAG  
GTGGTGAGCACCGACGAGTACGTGGCCCGACCAACATCTACTACCACGCCGGCACCGC  
CGCCTGCTGCCGTGGCCACCCCTACTTCCCCATCAAGAAGCCAAACAACAACAAGATC  
CTGGTGCCCAAGGTGAGCGGCCGTGCAGTACCGCGTGTCCGCATCCACCTGCCGACCCC  
AACAAAGTTCGGCTTCCCCGACACAAGCTTCTACAACCCCGACACCCAGCGCCTGGTGTGG  
GCCTGCCTGGCGTGGAGGTGGGCCGCCAGCCCTGGCGTGGCATCAGCGGCCAC  
CCCCTGCTGAACAAGCTGGACGACACCGAGAACGCCAGCGCCTACGCCGCCAACGCCGGC  
GTGGACAACCGCGAGTGCATCAGCATGGACTACAAGCAGACCCAGCTGTGCCTGATGGC  
TGCAAGCCTCCCATCGCGAGCACTGGGCAAGGGCAGCCCTGCACCAACGTGGCGTG  
AACCCCGGCCACTGCCCTCCCTGGAGCTGATCAACACCGTGATCCAGGACGGGACATG  
GTGGACACCGGCTTCGGCGCCATGGACTTCACCACCCCTGCAGGCCAACAGAGCGAGGTG  
CCCCTGGACATCTGCAACCAGCATCTGCAAGTACCCGACTACATCAAGATGGTGAGCGAG  
CCCTACGGCGACAGCCTGTTCTACCTGCGCCGAGCAGATGTTGTCGCCACCTG  
TTCAACCGGCCGGCGCCGTGGCGAGAACGTGCCGACGACCTGTACATCAAGGGCAGC  
GGCAGCACGCCAACCTGGCAGCAGCAACTACTCCCACTCCAGCGCAGCATGGT  
ACCAGCGACGCCAACCTTCAACAAGCCCTACTGGCTGCAGCGGCCAGGGCCACAAC  
AACGGCATCTGCTGGGGCAACCAAGCTGTTGACCGTGGGACACCACCCGAGCACC  
AACATGAGCCTGTGCCGCCATCAGCACCAAGCAGACCTACAAGAACACCAACTTC  
AAGGAGTACCTGCGCCACGGCGAGGAGTACGACCTGCAGTTCATCTTCAGCTGTGCAAG  
ATCACCTGACCGGCCACGTGATGACCTACATCCACAGCATGAACAGCACCATCCTGGAG  
GAUTGGAACTTCGGCCTGCAGCCCCCTCCCGCGGTACCCCTGGAGGACACCTACCGCTTC  
GTGACCAGCCAGGCCATGCCCTGCCAGAACACCCCTCCCGCTCCCAAGGGAGATCCC  
CTGAAGAAGTACACCTCTGGGAGGTGAACCTGAAGGAGAACGTTCAAGGCCGACCTGGAC  
CAGTCCCCCTGGGCCCAAGTTCTGCTGCAGGCCGGCTGAAGGCCAACGTTCAAGGCCAAC  
ACCCCTGGCAAGCGCAAGGCCACCCCAACCACAGCAGCACCAACCGCCAAGCGC  
AAGAAGCGCAAGCTGTAA

**FIG. 1**

SEQ.ID.NO.:2 Codon-Optimized HPV16 E1-G482D, W439R Mutant:

ATGGCCGACCCGCCGGCACCAACGGCGAGGAGGGCACCGGCTGCAACGGCTGGTTCTAC  
GTGGAGGCCGTGGTGGAGAAGAAGACCGGGCACGCCATCAGCGACGACGAGAACGAGAAC  
GACAGCGACACCGGGCGAGGACCTGGTGGACTTCATCGTAACGACAACGACTACCTGACC  
CAGGCCGAGACCGAGACCGCCCACGCCCTGTTACCGCCAGGAGGCCAAGCAGCACCGC  
GACGCCGTGCAGGTGCTGAAGCGCAAGTACCTGGGAGGCCCTGAGCGACATCAGCGGC  
TGCCTGACAACAAACATCAGCCCCGCCCTGAAGGCCATCTGCATCGAGAACGAGGCC  
GCCGCCAACGCGCCGCTGTTGAGAGCGAGGACAGCGGCTACGGCAACACCGAGGTGGAG  
ACCCAGCAGATGCTGCAGGTGGAGGGCCACGAGACCGAGACCCCTGCAGCCAGTAC  
AGCGGCCGGCAGCGGGCGCTGCAGCCAGTACAGCAGCGCAGCGCCGGCGAGGGCGTG  
AGCGAGCGCCACACCATCTGCCAGACCCCTTGACCAACATCCTGAACGTGCTGAAGACC  
AGCAACGCCAACGCCATGCTGCCAAGTTCAAGGAGCTGTACGGCGTGAGCTTCAGC  
GAGCTGGTGCCTGCCCTCAAGAGCAACAAAGAGCACCTGCTGCAGACTGGTGATGCC  
TTCGGCCTGACCCCCAGCATGCCAGACAGCATCAAGACCCCTGCTGCAGCAGTACTGCC  
TACCTGCACATCCAGAGCCTGCCCTGCAGCTGGGAGCTGGTGCTGCTGCTGGTGCGC  
TACAAGTGCAGCAAGAACCGCGAGACCATCGAGAACGCTGCTGAGCAAGCTGCTGCGTG  
AGCCCCATGTGCATGATGATCGAGCCTCCAAAGCTCGCAGCACCGCCGCCCTGTAC  
TGGTACAAGACCGGCATCAGAACATCAGCAGGTGTACGGCGACACCCCGAGTGGATC  
CAGCGCCAGACCGTGCAGCACAGCTTCAACGACTGCACCTTGAGCTGAGCCAGATG  
GTGCAGTGGCCTACGACAACGACATCGTGGACGACAGCAGATGCCATCAAGTACGCC  
CAGCTGGCCGACACCAACAGCAACGCCAGCGCCTCCCTGAAGAGCAACAGCCAGGCCAAG  
ATCGTGAAGGACTGCCACCATGTGCCCACTACAAGCGCCGAGAACGAGCACGATG  
AGCATGAGCCAGTGGATCAAGTACCGCTGCAGCCGTGGACGACGGCGCGACCGCAAG  
CAGATCGTGTGATGTTCTGCCTGCAGGGCTTCCATGAGCTTCCCTGACCGCCCTG  
AAGCGCTTCCCTGCAGGGCATCCCCAAGAACGACTGCATCCTGCTGTACGGCGCCAAAC  
ACCGACAAGAGCCTGTTGGCATGAGCCTGATGAAGTTCCCTGCAGGGCAGCGTGATCTGC  
TTCGTGAACAGCAAGAGCCACTTCTGGCTGCAGCCCTGGCCGACGCCAAGATCGGATG  
CTGGACGACGCCACCGTGCCTGCTGGAACATCGACGACAACCTGCGCAACGCCCTG  
GACGGCAACCTGGTGGAGCATGGACGTGAAGCACGCCCTGGTGCAGCTGAAGTGCC  
CCCTGCTGATCACCAGCAACATCAACGCCGGCACCGACAGCGCTGGCCCTACCTGCAC  
AACCGCCTGGTGGTGTTCACCTCCCCAACGAGTTCCCTTGACGAGAACGGTAACCC  
GTGTACGAGCTGAACGACAAGAACGACTGGAAGAGCTCTTGACGCCGACCTGGAGGCC  
AGCCTGCACGAGGACGGAGAACGGAGAACGACGGCGACAGCCTGCCACCTCAAGTGC  
GTGAGCGGCCAGAACACCAACACCCCTGTAA

FIG.2

SEQ. ID. NO.:3 Sequence of the Codon-Optimized HPV16E2-E39A, I73A Mutant:

ATGGAGACCCTGTGCCAGCGCTGAACGTGTGCCAGGACAAGATCCTGACCCACTACGAG  
AACGACAGCACCACCTGCGCACCACATCGACTACTGGAAGCACATGCGCCTGGCCTGC  
GCCATCTACTACAAGGCCCGCGAGATGGGCTTCAAGCACATCAACCACCAGGTGGTGC  
ACCCTGGCCGTGAGCAAGAACAAAGGCCCTGCAGGCCGCGAGCTGCAGCTGACCCCTGGAG  
ACCATCTACAAACAGCCAGTACAGCAACGAGAAGTGGACCCCTGCAGGACGTGAGCCTGGAG  
GTGTACCTGACCGCCCCCACCAGCTGCATCAAGAACGACGGCTACACCGTGGAGGTGCAG  
TTCGACGGCGACATCTGCAACACCATGCACTACACCAACTGGACCCACATCTACATCTGC  
GAGGAGGCCAGCGTACCGTGGTGGAGGGCCAGGTGGACTACTACGGCCTGTACTACGTG  
CACGAGGGCATCCGACCTACTTCGTGCAGTTCAAGGACGACGCCGAGAACAGTACAGCAAG  
AACAAAGGTGTGGGAGGTGCACGCCGGCCAGGTGATCCTGTGCCCAACCAAGCGTGTTC  
AGCAGCAACGAGGTGAGCAGCCCCGAGACCATCCGCCAGCACCTGGCCAACCACAGCGCC  
GCCACCCACACCAAGGCCGTGGCCCTGGGCACCGAGGAGACCCAGACCACCATCCAGCGC  
CCCCGCAGCGAGCCGACACCGGCAACCCCTGCCACACCACCAAGCTGCTGCACCGCGAC  
AGCGTGGACAGCGCCCCCATCTGACCGCCTCAACAGCAGCCACAAGGGCCGATCAAC  
TGCAACAGCAACACCAACCCCCCATCGTGCACCTGAAGGGCGACGCCAACACCTGAAGTGC  
CTCGCCTACCGCTTCAAGAACGACTGCAAGCTGTACACCGCCGTGAGCAGCACCTGGCAC  
TGGACCGGCCACAACGTGAAGCACAAGAGCGCCATCGTACCCCTGACCTACGACAGCGAG  
TGGCAGCGCGACCAGTTCTGAGCCAGGTGAAGATCCCCAAGACCATACCGTGAGCACC  
GGCTTCATGAGCATCTAA

**FIG.3**

SEQ. ID. NO.:4 Codon-Optimized HPV16E7-C24G, E26 Mutant:

ATGCACGGCGACACCCCCACCCCTGCACGAGTACATGCTGGACCTGCAGCCGAGACCACC  
GACCTGTACGGCTACGGCCAGCTGAACGACAGCAGCGAGGAGGAGGACGAGATCGACGGC  
CCCGCCGGCCAGGCCAGGCCGACCGCGCCACTAACATCGTACCTCTGCTGCAAG  
TGCACAGCACCCCTGCGCCTGTGCGTGCAGAGCACCCACGTGGACATCCGACCCCTGGAG  
GACCTGCTGATGGGCACCCCTGGGCATCGTGTGCCCATCTGCAGCCAGAACGCCCTAA

**FIG.4**

SEQ.ID.NO.:5 Codon-Optimized HPV6a E7 Gene:

ATGCACGGCCGCCACGTGACCCCTGAAGGACATCGTGTGGACCTGCAGCCTCCGACCCC  
GTGGGCCTGCACTGCTACGAGCAGCTGGTGGACAGCAGCGAGGACGAGGTGGACGAGGTG  
GACGGCCAGGACAGCCAGCCCTGAAGCAGCACTTCCAGATCGTGTGACCTGCTGCGGC  
TGCACAGAACGTGCGCCTGGTGGTGCAGTCACCGAGACCGACATCCGCGAGGTGCAG  
CAGCTCCTGCTGGTACCCCTGAACATCGTGTGCCCATCTGCGCTCCAAGACCTAA

**FIG.5**

SEQ.ID.NO.:6 Codon-Optimized HPV18 E7 Gene:

ATGCACGGCCCCAAGGCCACCCCTGCAGGACATCGTGTGCACCTGGAGCCCCAGAACGAG  
ATCCCCGTGGACCTGCTGTGCCACGAGCAGCTGAGCGACAGCGAGGAGGAGAACGACGAG  
ATCGACGGCGTGAACCACCAAGCACCTGCCGCTCGCAGGGCCGAGCCCCAGCGGCCACACC  
ATGCTGTGCATGTGCTGCAAGTGCAGGGCCGCATCGAGCTGGTGGAGAGCAGCGCT  
GACGACCTGCGCGCCTCCAGCAGCTGTTCTGAACACCCCTGAGCTTCGTGTGCCCTGG  
TGCGCCAGCCAGCAGTAA

**FIG.6**

SEQ.ID.NO.:7 Codon-Optimized HPV6a E2 Gene:

ATGGAGGCCATGCCAAGCGCTGGACGCCCTGCCAGGAGCAGCTGCTGGAGCTGTACGAG  
GAGAACAGCACCGACCTGCACAAGCACGTGCTGCAGTGGAGTCATGCCACGAGAGC  
GTGCTGCTGTACAAGGCCAACAGCAGATGGCCTGAGCCACATCGGCATGCAGGTGGTGCCT  
CCTCTGAAGGTGAGCGAGGCCAACAGGCCCACACGCCATCGAGATGCAGATGCACCTCGAG  
AGCCTGCTGCGACCGAGTACAGCATGGAGCCCTGGACCCCTGCAGGAGACCAGCTACGAG  
ATGTGGCAGACCCCTCCAAGCGCTGCTCAAGAACAGCAGTGGACTACGTGGTGGACCGACGTGAAG  
TTCGACGGCTGCGCAACAAACACCATGGACTACGTGGTGTGGACCGACGTGTACGTGCAG  
GACAACGACACCTGGGTGAAGGTGCACAGCATGGTGGACGCCAAGGGCATCTACTACACC  
TGTGGCCAGTTCAAGACCTACTACGTGAACCTCGTGAAGGAGGCCGAGAAGTACGGCAGC  
ACCAAGCACTGGGAGGTGTGCTACGGCAGCACCGTATCTGAGCCCCGCTAGCGTGAGC  
AGCACCACCCAGGAGGTGAGCATCCCCGAGAGCACCACCTACACTCCCAGGCCAGACCAGC  
ACCCCTGGTGAGCAGCACCAAGGAGGCCGTGAGACCCCTCTCGCAAGCGCGCC  
CGCGCGTGCAGCAGAGCCCCCTGCAACGCCCTGTGCGTGGCCACATCGGCCCCGTGGAT  
AGCGGAACCAACCTGATCACCAACAACCACGACCAGCACCGCCGCAACAAACAGC  
AACAGCAGCGCCACTCCCCTCGTGCAGTTCCAGGGCGAGAGCAACTGCCTGAAGTGCTTC  
CGCTACCGCCTGAACGATGCCACCGCCACCTGTTGACCTGATCAGCAGCACCTGGCAC  
TGGGCCAGCAGCAAGGCTCCCCACAAGCACGCCATCGTACCGTGAACCTACGACAGCGAG  
GAGCAGCGCCAGCAGTCTGGACGTGGTAAGATCCCTCCACCATCAGCCACAAGCTG  
GGCTTCAATGAGCCTGCACCTGCTGTAA

**FIG.7**

SEQ. ID. NO.: 8 Codon-Optimized HPV18 E2 Gene:

ATGCAGACTCCCAAGGAGACCTGAGCGAGCGCCTGAGCGCCCTGCAGGACAAGATCATC  
GACCACTACGAGAACGACAGCAAGGACATCGACAGCCAGATCCAGTACTGGCAGCTGATC  
CGCTGGGAGAACGCCATCTTCTCGCCGCTCGCAGCAGGGATCCAGACCCCTGAACCAC  
CAGGTGGTGCCCGCCTACAACATCAGCAAGAGCAAGGCCACAAGGCCATCGAGCTGCAG  
ATGGCCCTGCAGGGCCTGGCCCAGAGCGCCTACAAGACCGAGGACTGGACCCCTGCAGGAC  
ACCTGCGAGGAGCTGTGGAACACCGAGGCCACCCACTGCTTAAGAAGGGAGGCCAGACC  
GTGCAGGTGTACTTCGACGGCAACAAGGACAATGCATGAACACTACGTGGCCTGGGACAGC  
GTGTACTACATGACCGACGCCGGCACCTGGGACAAGACCAGGCCACCTGCGTGAGCCACCGC  
GGCCTGTACTACGTGAAGGAGGGCTACAACACCTTACATCGAGTTCAAGAGCGAGTGC  
GAGAAGTACGGCAACACCGGCACCTGGGAGGTGCACTTCGGCAACAACGTGATCGACTGC  
AACGACAGCATGTGCAGCACCGACGACACCGTGAGCGCCACCCAGCTGGTGAAGCAG  
CTGCAGCACACTCCAGCCCTACAGCAGCACCGTGAGCGTGGCACCAGCCAAGACCTAC  
GGCCAGACCAGCGCCGCCACTCGCCCTGGCCACTGCGGCCTGGCCGAGAAGCAGCACTGC  
GGGCCCGTGAACCCCTGCTGGCGCCGCCACCGCAACAACAGCGCCGAAG  
CTGTGCAGCGGCAACACCAACTCCCATCCACCTGAAGGGCGACCGCAACAGCCTGAAG  
TGCTGCGGTACCGCCTGCGCAAGCACAGCGACCAACTACCGCGACATCAGCAGCACCTGG  
CACTGGACCGCGCCGGAACGAGAAGACCGGATCCTGACCGTGACCTACCACAGCGAG  
ACCCAGCGCACCAAGTTCTGAACACCGTGGCCATCCCCGACAGCGTGCAGATCCTGGTG  
GGCTACATGACCATGTAA

**FIG. 8**

Comparison of protein expression of  
native and synthetic HPV16 L1 genes

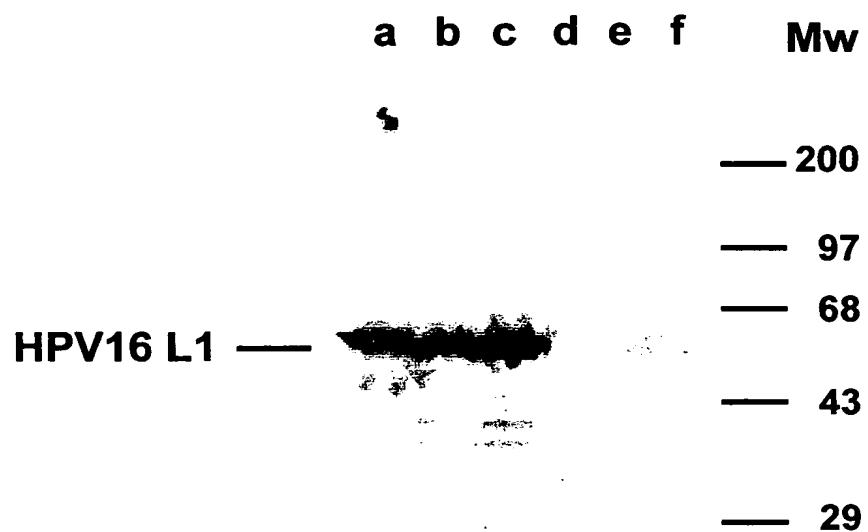


FIG.9

Comparison of protein expression  
of native and synthetic HPV 16 E1 genes

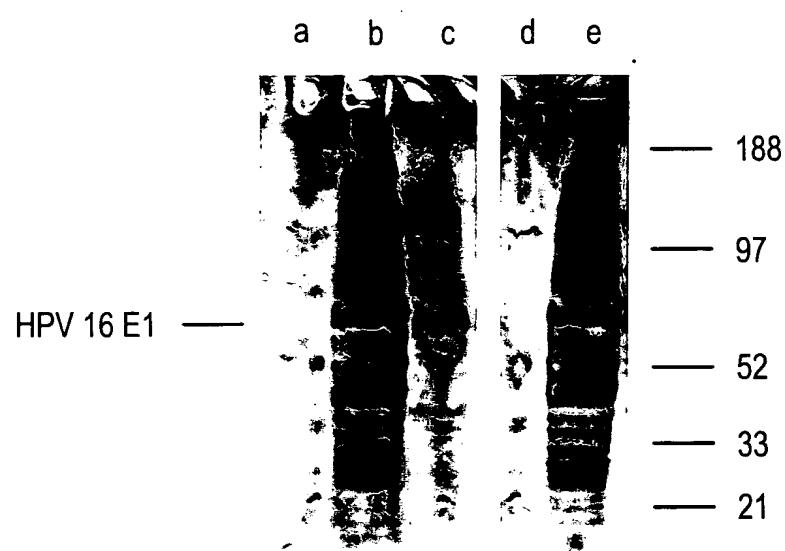
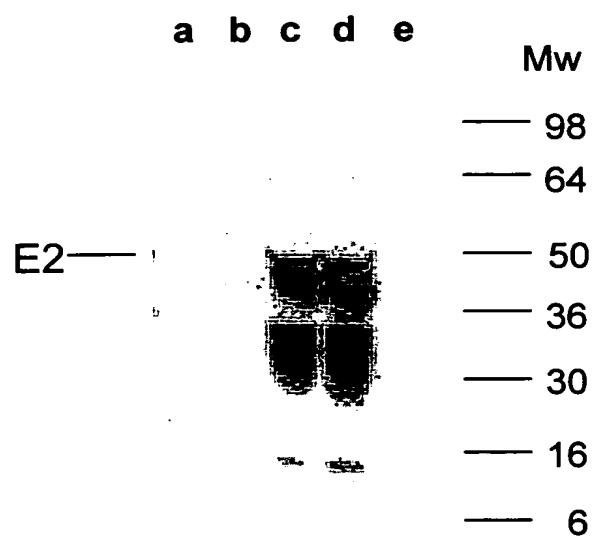


FIG. 10

9/28

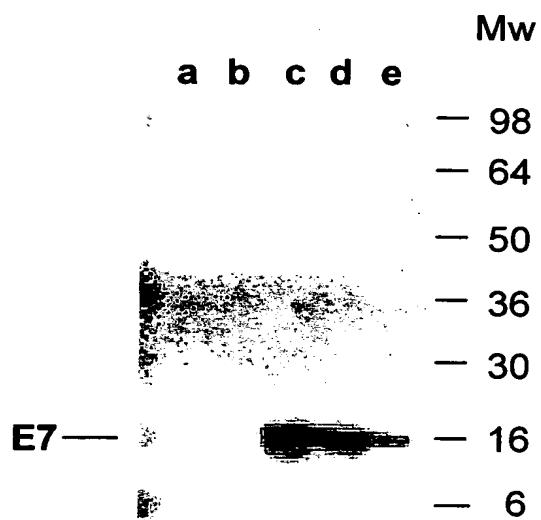


- a. mock
- b. lacZ
- c. synthetic 16 E2 isolate 6
- d. synthetic 16 E2 isolate 11
- e native 16 E2

FIG. 11

10/28

Comparison of protein expression of native and synthetic HPV16 E7 genes



- a. mock
- b. lacZ
- c. synthetic HPV16 E7 isolate 2
- d. synthetic HPV16 E7 isolate 4
- e. native HPV16 E7

FIG.12

11/28

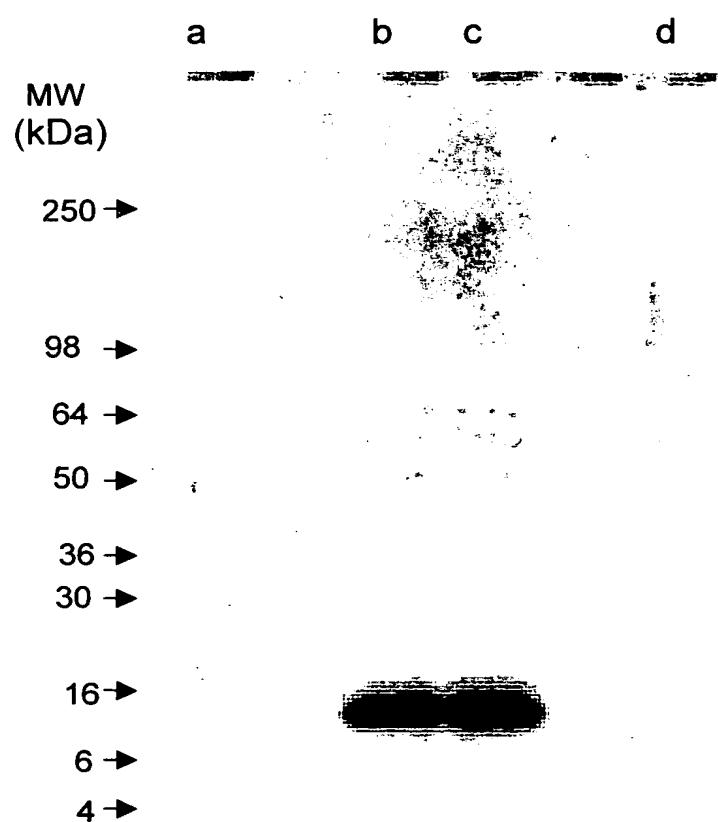


FIG.13

12/28

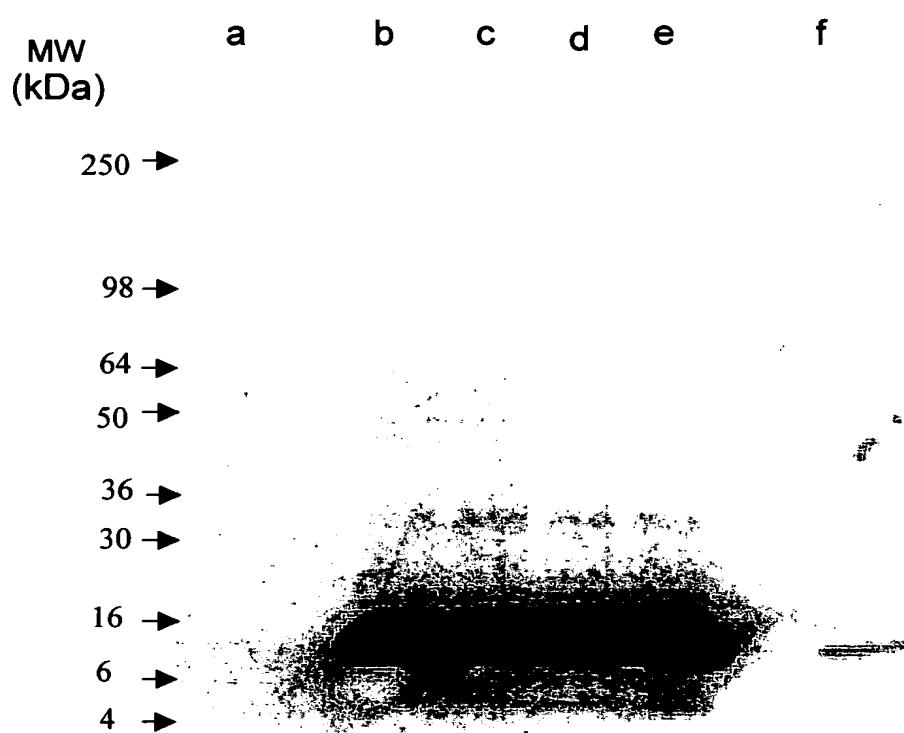


FIG.14

## Expression of synthetic HPV 6 E2 gene

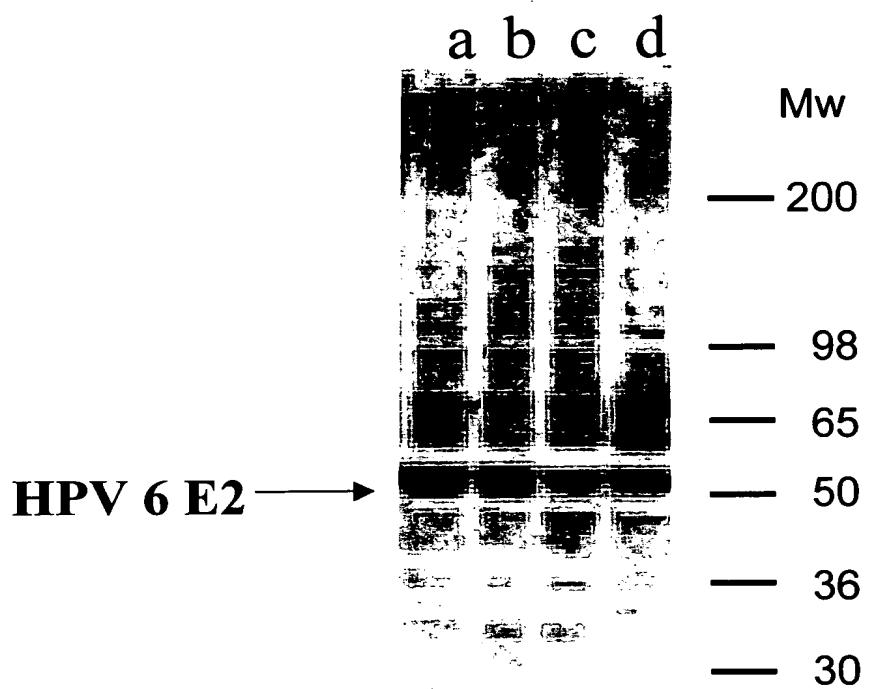


FIG. 15

## Expression of synthetic HPV 18 E2 gene

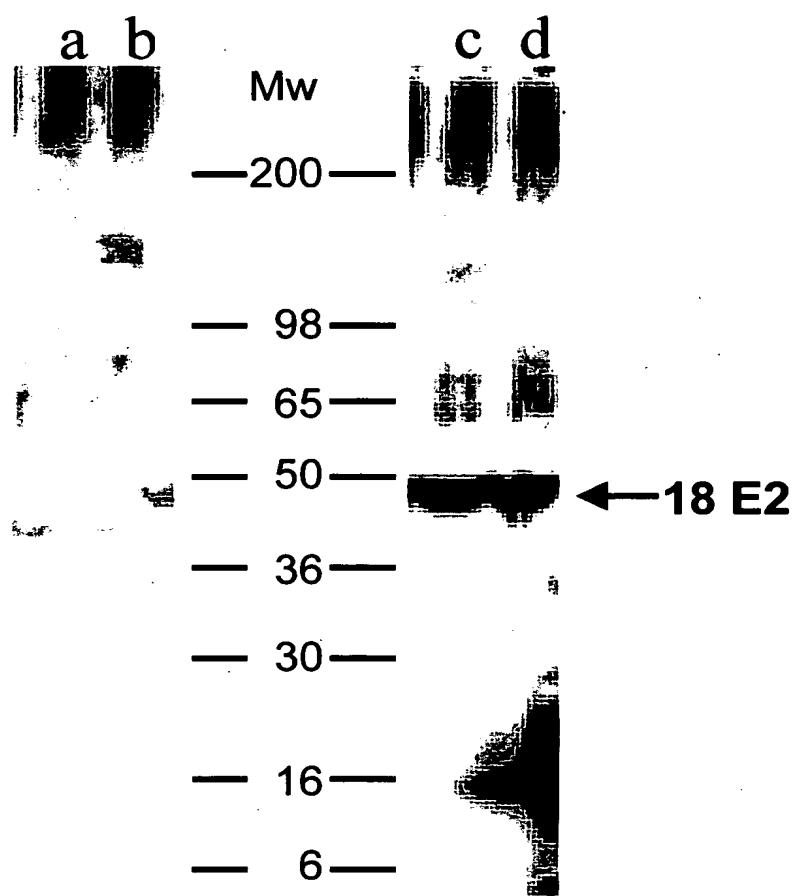


FIG. 16

HPV16 L1 Gene-Building Oligomers

MN4A1 (SEQ.ID.NO:9) 5' ATG AGC CTG TGG CTG CCC AGC GAG GCC ACC GTG TAC CTG CCT CCC GTG CCC GTG AGC AAG GTG GTG AGC ACC GAC GAG TAC GTG GCC CGC ACC AAC ATC TAC TAC CAC GCC GGC ACC AGC CGC CTG CTG 3'

MN4A3 (SEQ.ID.NO:10) 5' CGC ATC CAC CTG CCC GAC CCC AAC AAG TTC GGC TTC CCC GAC ACA AGC TTC TAC AAC CCC GAC ACC CAG CGC CTG GTG TGG GCC TGC GTG GGC GTG GAG GTG GGC CGC GGC CAG CCC CTG GGC GTG GGC 3'

MN4A5 (SEQ.ID.NO:11) 5' GAG TGC ATC ATC AGC ATG GAC TAC AAG CAG ACC CAG CTG TGC CTG ATC GGC TGC AAG CCT CCC ATC GGC GAG CAC TGG GGC AAG GGC AGC CCC TGC ACC AAC GTG GCC GTG AAC CCC GGC GAC TGC CCT CCC 3'

MN4A7 (SEQ.ID.NO:12) 5' GCC AAC AAG AGC GAG GTG CCC CTG GAC ATC TGC ACC AGC ATC TGC AAG TAC CCC GAC TAC ATC AAG ATG GTG AGC GAG CCC TAC GGC GAC AGC CTG TTC TTC TAC CTG CGC CGC GAG CAG ATG TTC GTG CGC 3'

MN4A9 (SEQ.ID.NO:13) 5' GCC AGC AGC AAC TAC TTC CCC ACT CCC AGC GGC AGC ATG GTG ACC AGC GAC GCC CAA ATC TTC AAC AAG CCC TAC TGG CTG CAG CGC GCC CAG GGC CAC AAC AAC GGC ATC TGC TGG GGC AAC CAG CTG 3'

MN4A11 (SEQ.ID.NO:14) 5' GAG TAC CTG CGC CAC GGC GAG GAG TAC GAC CTG CAG TTC ATC TTC CAG CTG TGC AAG ATC ACC CTG ACC GCC GAC GTG ATG ACC TAC ATC CAC AGC ATG AAC AGC ACC ATC CTG GAG GAC TGG AAC TTC GGC CTG 3'

MN4A13 (SEQ.ID.NO:15) 5' GCT CCC AAG GAG GAT CCC CTG AAG AAG TAC ACC TTC TGG GAG GTG AAC CTG AAG GAG AAG TTC AGC GCC GAC CTG GAC CAG TTC CCC CTG GGC CGC AAG TTC CTG CTG CAG GCC CTG AAG GCC AAG CCC AAG 3'

MN4A2 (SEQ.ID.NO:16) 5' GTT GGG GTC GGG CAG GTG GAT GCG GAA CAC GCG GTA CTG CAG GCC GCT CAC CTT GGG CAC CAG GAT CTT GTT GTT GGG CTT CTT GAT GGG GAA GTA GGG GTG GCC CAC GGC CAG CAG GCG GCT GGT GCC GGC 3'

**FIG.17A**

16/28

MN4A4 (SEQ. ID.NO:17) 5' CTT GTA GTC CAT GCT GAT GCA CTC GCG GTT GTC CAC GCC GGC GTT GGC GGC GTA GGC GCT GGC GTT CTC GGT GTC GTC CAG CTT GTT CAG CAG GGG GTG GCC GCT GAT GCC CAC GGC CAG GGG CTG GCC GCG 3'

MN4A6 (SEQ. ID.NO:18) 5' CAG GGG CAC CTC GCT CTT GGC CTG CAG GGT GGT GAA GTC CAT GGC GCC GAA GGC GGT GTC CAC CAT GTC GCC GTC CTG GAT CAC GGT GTT GAT CAG CTC CAG GGG AGG GCA GTC GCC GGG GTT CAC 3'

MN4A8 (SEQ. ID.NO:19) 5' GGG AGT GGG GAA GTA GTT GCT GCT GGC CAG GTT GGC GGT GCT GCC GCT GGC CTT GAT GTA CAG GTC GTC GGG CAC GTT CTC GCC CAC GGC GCC GGC GCG GTT GAA CAG GTG GCG CAC GAA CAT CTG CTC GCG 3'

MN4A10 (SEQ. ID.NO:20) 5' CTC CTC GCC GTG GCG CAG GTA CTC CTT GAA GTT GGT GTT CTT GTA GGT GGT CTC GCT GGT GCT GAT GGC GGC GCA CAG GCT CAT GTT GGT GCT GCG GGT GGT GTC CAC CAC GGT CAC GAA CAG CTG GTT GCC CCA GCA GAT GCC 3'

MN4A12 (SEQ. ID.NO:21) 5' CTT CAG GGG ATC CTC CTT GGG AGC GGG AGG GGT GTG CTT CTG GCA GGC GAT GGC CTG GCT GGT CAC GAA GCG GTA GGT GTC CTC CAG GGT ACC GCC GGG AGG GGG CTG CAG GCC GAA GTT CCA GTC CTC CAG 3'

MN4A14 (SEQ. ID.NO:22) 5' CAC TAG AGA TCT GAA TTC TTA CAG CTT GCG CTT CTT GCG CTT GGC GGT GGT GCT GGT GCT GGT GGT GGG GGT GGC CTT GCG CTT GCC CAG GGT GAA CTT GGG CTT GGC CTT CAG GCC GGC 3'

MN595 (SEQ. ID.NO:23) 5' CGC GGC CAG CCC CTG GGC GTG 3'

MN596 (SEQ. ID.NO:24) 5' GCC CAC GCC CAG GGG CTG GCC GCG 3'

MN597 (SEQ. ID.NO:25) 5' GCC AAC AAG AGC GAG GTG CCC 3'

MN598 (SEQ. ID.NO:26) 5' CAG GGG CAC CTC GCT CTT GTT GGC 3'

MN599 (SEQ. ID.NO:27) 5' GCC AGC AGC AAC TAC TTC CCC AC 3'

MN600 (SEQ. ID.NO:28) 5' GGG AGT GGG GAA GTA GTT GCT GC 3'

MN601 (SEQ. ID.NO:29) 5' CTG GAG GAC TGG AAC TTC GGC CTG 3'

MN602 (SEQ. ID.NO:30) 5' CAG GCC GAA GTT CCA GTC CTC CAG 3'

MN603 (SEQ. ID.NO:31) 5' CAC TAG AGA TCT GAA TTC TTA CAG C 3'

MN604 (SEQ. ID.NO:32) 5' CAT CTC AGA TCT GCC ACC ATG AGC CTG TGG CTG CCC AG 3'

FIG.17B

HPV16E1 Gene-building Oligomers

MN605 (SEQ.ID.NO:33) 5' ATG GCC GAC CCC GCC GGC ACC AAC GGC GAG GAG GGC ACC GGC TGC AAC GGC TGG TTC TAC GTG GAG GCC GTG GTG GAG AAG AAG ACC GGC GAC GCC ATC AGC GAC GAC GAG AAC GAC AGC GAC 3'

MN606 (SEQ.ID.NO:34) 5' GTG CTG CTT GGC CTC CTG GGC GGT GAA CAG GGC GTG GGC GGT CTC GGT CTC GGC CTG GGT CAG GTA GTC GTT GTC GTC GTT CAC GAT GAA GTC CAC CAG GTC CTC GCC GGT GTC GCT GTC GTT CTC GTC GTC 3'

MN607(SEQ.ID.NO:35) 5' GCC CAG GAG GCC AAG CAG CAC CGC GAC GCC GTG CAG GTG CTG AAG CGC AAG TAC CTG GGC AGC CCC CTG AGC GAC ATC AGC GGC TGC GTC GAC AAC AAC ATC AGC CCC CGC CTG AAG GCC ATC TGC ATC GAG 3'

MN608 (SEQ.ID.NO:36) 5' CTC GTG GCG GCC CTC CAC CTG CAG CAT CTG CTG GGT CTC CAC CTC GGT GTT GCC GTA GCC GCT GTC CTC GCT CTC GAA CAG GCG GCG CTT GGC GGC GCG GCT CTG CTT CTC GAT GCA GAT GGC CTT CAG GC 3'

MN609 (SEQ.ID.NO:37) 5' CAG GTG GAG GGC CGC CAC GAG ACC CCC TGC AGC CAG TAC AGC GGC GGC AGC GGC GGC TGC AGC CAG TAC AGC AGC GGC AGC GGC GGC GAG GGC GTG AGC GAG CGC CAC ACC ATC TGC CAG ACC 3'

MN610 (SEQ.ID.NO:38): 5' CTT GAA GGG GCG CAC CAG CTC GCT GAA GCT CAC GCC GTA CAG CTC CTT GAA CTT GGC CAG CAT GGC GGC CTT GGC GTT GCT GGT CTT CAG CAC GTT CAG GAT GTT GGT CAG AGG GGT CTG GCA GAT GGT GTG GCG 3'

MN611 (SEQ.ID.NO:39) 5' GAG CTG GTG CGC CCC TTC AAG AGC AAC AAG AGC ACC TGC TGC GAC TGG TGC ATC GCC GCC TTC GGC CTG ACC CCC AGC ATC GCC GAC AGC ATC AAG ACC CTG CTG CAG CAG TAC TGC TAC CTG CAC ATC CAG 3'

MN612 (SEQ.ID.NO:40) 5' CAT GGG GCT CAC GCA CAG CAG CTT GCT CAG CAG CTT CTC GAT GGT CTC GCG GTT CTT GCC GCA CTT GTA GCG CAC CAG CAG CAC CAC CAT GCC CCA GCT GCA GGC CAG GCT CTG GAT GTG CAG GTA CAG GCA G 3'

**FIG.18A**

MN613 (SEQ.ID.NO:41) 5' CTG CTG TGC GTG AGC CCC ATG TGC ATG ATG ATC GAG CCT CCC AAG CTT CGC AGC ACC GCC GCC CTG TAC TGG TAC AAG ACC GGC ATC AGC AAC ATC AGC GAG GTG TAC GGC GAC ACC CCC GAG TGG ATC 3'

MN614 (SEQ.ID.NO:42) 5' GGC GAT CTC GCT GTC GTC CAC GAT GTC GTT GTC GTA GGC CCA CTG CAC CAT CTG GCT CAG CTC GAA GGT GCA GTC GTT GAA GCT GTG CTG CAG CAC GGT CTG GCG CTG GAT CCA CTC GGG GGT GTC GCC 3'

MN615 (SEQ.ID.NO:43): 5' GTG GAC GAC AGC GAG ATC GCC TAC AAG TAC GCC CAG CTG GCC GAC ACC AAC AGC AAC GCC AGC GCC TTC CTG AAG AGC AAC AGC CA GGC CAA GAT CGT GAA GGA CTG CGC CAC CAT GTG CCG CCA CTA C 3'

MN616 (SEQ.ID.NO:44) 5' GTA GCG CAG GAA CAT CAC GAT CTG CTT GCG GTC GCC GCC GTC GTC CAC GCG GTC GCA GCG GTA CTT GAT CCA CTG GCT CAT GCT CAT CTG CTT CTT CTC GGC GCG CTT GTA GTG GCG GCA CAT GGT GGC 3'

MN617 (SEQ.ID.NO:45) 5' CAG ATC GTG ATG TTC CTG CGC TAC CAG GGC GTG GAA TTC ATG AGC TTC CTG ACC GCC CTG AAG CGC TTC CTG CAG GGC ATC CCC AAG AAG AAC TGC ATC CTG CTG TAC GGC GCC AAC ACC GAC AAG 3'

MN618 (SEQ.ID.NO:46) 5' GCC GAT CTT GGC GTC GGC CAG GGG CTG CAG CCA GAA GTG GCT CTT GCT GTT CAC GAA GCA GAT CAC GCT GCC CTG CAG GAA CTT CAT CAG GCT CAT GCC GAA CAG GCT CTT GTC GGT GTT GGC GGC GCCG 3'

MN619 (SEQ.ID.NO:47) 5' CTG GCC GAC GCC AAG ATC GGC ATG CTG GAC GAC GCC ACC GTG CCC TGC TGG AAC TAC ATC GAC GAC AAC CTG CGC AAC GCC CTG GAC GGC AAC CTG GTG AGC ATG GAC GTG AAG CAC CGC CCC CTG GTG 3'

MN620 (SEQ.ID.NO:48) 5' GAA CTC GTT GGG GAA GGT GAA CAC CAC CAG GCG GTT GTG CAG GTA GGG CCA GCG GCT GTC GGT GCC GGC GTT GAT GTT GCT GGT GAT CAG CAG GGG AGG GCA CTT CAG CTG CAC CAG GGG GCG GTG CTT CAC 3'

## FIG.18B

19/28

MN621 (SEQ.ID.NO:49) 5' GTG TTC ACC TTC CCC AAC GAG TTC CCC TTC GAC GAG AAC GGT AAC CCC GTG TAC GAG CTG AAC GAC AAG AAC TGG AAG AGC TTC TTC AGC CGC ACC TGG AGC CGC CTG AGC CTG CAC GAG GAC GAG 3'

MN622 (SEQ.ID.NO:50) 5' CAT GAG AGA TCT TTA CAG GGT GTT GGT CTG GCC GCT CAC GCA CTT GAA GGT GGG CAG GCT GTC GCC GTC GTT CTC CTT GTC CTC GTC CTC GTG CAG GCT CAG 3'

MN623 (SEQ.ID.NO:51) 5' GCC TGA AGG CCA TCT GCA TCG AG 3'

MN624 (SEQ.ID.NO:52) 5' CTC GAT GCA GAT GGC CTT CAG GC 3'

MN625 (SEQ.ID.NO:53) 5' GAG CTG GTG CGC CCC TTC AAG 3'

MN626 (SEQ.ID.NO:54) 5' CTT GAA GGG GCG CAC CAG CTC 3'

MN627 (SEQ.ID.NO:55) 5' CTG CTG TGC GTG AGC CCC ATG 3'

MN628 (SEQ.ID.NO:56) 5' CAT GGG GCT CAC GCA CAG CAG 3'

MN629 (SEQ.ID.NO:57) 5' GCC ACC ATG TGC CGC CAC TAC 3'

MN630 (SEQ.ID.NO:58) 5' GTA GTG GCG GCA CAT GGT GGC 3'

MN631 (SEQ.ID.NO:59) 5' CTG GCC GAC GCC AAG ATC GGC 3'

MN632 (SEQ.ID.NO:60) 5' GCC GAT CTT GGC GTC GGC CAG 3'

MN633 (SEQ.ID.NO:61) 5' GTG TTC ACC TTC CCC AAC GAG TTC 3'

MN634 (SEQ.ID.NO:62) 5' GAA CTC GTT GGG GAA GGT GAA CAC 3'

MN635 (SEQ.ID.NO:63) 5' CAT GAG AGA TCT TTA CAG GGT GTT G 3'

MN636 (SEQ.ID.NO:64) 5' CAT CTC AGA TCT GCC ACC ATG GCC GAC CCC GCC GGC AC 3'

FIG.18C

20/28

Oligonucleotides used in the generation of synthetic HPV 16 E2

13856-307-2A (SEQ.ID.NO:65) 5' ATG GAG ACC CTG TGC CAG CGC CTG AAC GTG TGC CAG GAC AAG ATC CTG ACC CAC TAC GAG AAC GAC AGC ACC GAC CTG CGC GAC CAC ATC GAC TAC TGG 3'

13856-307-2C (SEQ.ID.NO:66) 5' CCA CCA GGT GGT GCC CAC CCT GGC CGT GAG CAA GAA CAA GGC CCT GCA GGC CGC CGA GCT GCA GCT GAC CCT GGA GAC GAT CTA CAA CAG CCA GTA CAG CAA CG 3'

13856-307-2E (SEQ.ID.NO:67) 5' CCG GCT GCA TCA AGA AGC ACG GCT ACA CCG TGG AGG TGC AGT TCG ACG GCG ACA TCT GCA ACA CCA TGC ACT ACA CCA ACT GGA CCC ACA TTT ACA TCT GTG AGG AGG 3'

13856-307-2G (SEQ.ID.NO:68) 5' CGT GCA CGA GGG GAT CCG CAC CTA CTT CGT GCA GTT CAA GGA CGA CGC CGA GAA GTA CAG CAA GAA CAA GGT GTG GGA GGT GCA CGC CGG AGG CCA GGT GAT CC 3'

13856-307-2I (SEQ.ID.NO:69) 5' GGC CAA CCA CAG CGC CGC CAC CCA CAC CAA GGC CGT GGC CCT GGG CAC CGA GGA GAC CCA GAC CAC AAT CCA GCG CCC TCG CAG CGA GCC CGA CAC CGG CAA CCC CTG CC 3'

13856-307-2K (SEQ.ID.NO:70) 5' GCC ACA AGG GCC GGA TCA ACT GCA ACA GCA ACA CCA CCC CTA TCG TGC ACC TGA AGG GCG ACG CCA ACA CCC TGA AGT GCC TGC GGT ACC GCT TCA AGA AGC ACT GC 3'

13856-307-2B (SEQ.ID.NO:71) 5' CCA GGG TGG GCA CCA CCT GGT GGT TGA TGT GCT TGA AGC CCA TCT CGC GGG CCT TGT AGT AGA TGG CGC AGG CCA GGC GCA TGT GCT TCC AGT CGA TGT GGT CGC GCA GG 3'

13856-307-2D (SEQ.ID.NO:72) 5' GCC GTG CTT CTT GAT GCA GCC GGT AGG GGC GGT CAG GTA CAC CTC CAG GCT CAC GTC CTG CAG GGT CCA CTT CTC GTT GCT GTA CTG GCT GTT GTA GAT CG 3'

13856-307-2F (SEQ.ID.NO:73) 5' GGT GCG GAT CCC CTC GTG CAC GTA GTA CAG GCC GTA GTA GTC CAC CTG GCC CTC CAC CAC GGT CAC GCT GGC CTC CTC ACA GAT GTA AAT GTG GGT CC 3'

13856-307-2H (SEQ.ID.NO:74) 5' GGG TGG CGG CGC TGT GGT TGG CCA GGT GCT GGC GGA TCG TCT CGG GGC TGC TCA CCT CGT TGC TGC TGA ACA CGC TGG TGG GGC ACA GGA TCA CCT GGC CTC CGG CGT GC 3'

FIG.19A

13856-307-2J (SEQ.ID.NO:75) 5' GCA GTT GAT CCG GCC CTT GTG GCT GCT GTT GAA GGC GGT CAG GAT AGG GGC GCT GTC GAC GCT GTC GCG GTG CAG CAG CTT GGT GGT GTG GCA GGG GTT GCC GGT GTC GGG 3'

13856-307-2L (SEQ.ID.NO:76) 5' CGT AGG TCA GGG TCA CGA TAG CGC TCT TGT GCT TCA CGT TGT GGC CGG TCC AGT GCC AGG TGC TGC TCA CGG CGG TGT ACA GCT TGC AGT GCT TCT TGA AGC GGT ACC GC 3'

13856-307-2M (SEQ.ID.NO:77) 5' TTT AGA TGC TCA TGA AGC CGG TGC TCA CGG TGA TGG TCT TGG GGA TCT TCA CCT GGC TCA GGA ACT GGT CGC GCT GCC ACT CGC TGT CGT AGG TCA GGG TCA CGA TAG CGC 3'

13856-307-2PA (SEQ.ID.NO:78) 5' CGA GCT GAT ATC GAA TTC AGA TCT GCC ACC ATG GAG ACC CTG TGC CAG CG 3'

13856-307-2PM (SEQ.ID.NO:79) 5' GGT TGC AGA TCT AGA CTC GAG TTT AGA TGC TCA TGA AGC CGG TGC 3'

13856-307-2PE (SEQ.ID.NO:80) 5' CCG GCT GCA TCA AGA AGC ACG 3'

13856-307-2PI (SEQ.ID.NO:81) 5' GGC CAA CCA CAG CGC CGC C 3'

13856-307-2PD (SEQ.ID.NO:82) 5' GCC GTG CTT CTT GAT GCA GCC 3'

13856-307-2PH (SEQ.ID.NO:83) 5' GGG TGG CGG CGC TGT GG 3'

13856-307-2PL (SEQ.ID.NO:84) 5' CGT AGG TCA GGG TCA CGA TAG C 3'

## FIG.19B

Oligonucleotides used in the generation of synthetic HPV 16 E7.

13856-307-7A (SEQ.ID.NO:85) 5' GGC CGG AGA TCT GAT ATC GAA TTC GCC ACC ATG CAC GGC GAC ACC CCC ACC CTG CAC GAG TAC ATG CTG GAC CTG CAG CCC GAG ACC ACC GAC CTG TAC GGC TAC GGC C 3'

13856-307-7C (SEQ.ID.NO:86) 5' GCC GAG CCC GAC CGC GCC CAC TAC AAC ATC GTG ACC TTC TGC TGC AAG TGC GAC AGC ACC CTG CGC CTG TGC GTG CAG AGC ACC CAC GTC GAC ATC CGC ACC CTG G 3'

13856-307-7B (SEQ.ID.NO:87) 5' GGG CGC GGT CGG GCT CGG CCT GGC CGG CGG GGC CGT CGA TCT CGT CCT CTT CCT CGC TGC TGT CGT TCA GCT GGC CGT AGC CGT ACA GGT CGG TGG 3'

13856-307-7D (SEQ.ID.NO:88) 5' CCG CGG CAG ATC TAG ACT CGA GTT TAG GGC TTC TGG CTG CAG ATT GGG CAC ACG ATT CCC AGG GTG CCC ATC AGC AGG TCC TCC AGG GTG CGG ATG TCG ACG TGG G 3'

13856-307-7PA (SEQ.ID.NO:89) 5' GGC CGG AGA TCT GAT ATC GAA TTC G 3'

13856-307-7PD (SEQ.ID.NO:90) 5' CCG CGG CAG ATC TAG ACT CG 3'

**FIG.20**

## Oligonucleotides Used for Construction of HPV6a E7 Gene

### A. DNA Template Oligos

LS207 (105-mer) (SEQ.ID.NO:91) 5' GTC ACA GAT CTG ATA TCG AAT TCC ACC ATG CAC GGC CGC CAC GTG ACC CTG AAG GAC ATC GTG CTG GAC CTG CAG CCT CCC GAC CCC GTG GGC CTG CAC TGC TAC 3'

LS208 (105-mer) (SEQ.ID.NO:92) 5' CTG GAA GTG CTG CTT CAG GGG CTG GCT GTC CTG GCC GTC CAC CTC GTC CAC CTC GTC CTC GCT GTC CAC CAG CTG CTC GTA GCA GTG CAG GCC CAC GGG GTC 3'

LS209 (107-mer) (SEQ.ID.NO:93) 5' CCA GCC CCT GAA GCA GCA CTT CCA GAT CGT GAC CTG CTG CTG CGG CTG CGA CAG CAA CGT GCG CCT GGT GGT GCA GTG CAC CGA GAC CGA CAT CCG CGA GGT GCA GC 3'

LS210 (102-mer) (SEQ.ID.NO:94) 5' CAG TCA GAT CTA GAG ATA TCT TTA GGT CTT GGG AGC GCA GAT GGG GCA CAC GAT GTT CAG GGT ACC CAG CAG GAG CTG CTG CAC CTC GCG GAT GTC GGT CTC 3'

### B. PCR Amplification Primers

LS211 (24-mer) (SEQ.ID.NO:95) 5' GTC ACA GAT CTG ATA TCG AAT TCC 3'

LS212 (26-mer) (SEQ.ID.NO:96) 5' CAG TCA GAT CTA GAG ATA TCT TTA GG 3'

**FIG.21**

Oligonucleotides Used for Construction of HPV18 E7 Gene

A. DNA Template Oligos

LS201 (109-mer) (SEQ.ID.NO:97) 5' GTC ACA GAT CTG ATA TCG AAT TCC ACC ATG CAC GGC CCC AAG GCC ACC CTG CAG GAC ATC GTG CTG CAC CTG GAG CCC CAG AAC GAG ATC CCC GTG GAC CTG CTG TGC C 3'

LS202 (111-mer) (SEQ.ID.NO:98) 5' GGG CTC GGC CCT GCG AGC GGG CAG GTG CTG GTG GTT CAC GCC GTC GAT CTC GTC GTT CTC CTC GCT GTC GCT CAG CTG CTC GTG GCA CAG CAG GTC CAC GGG GAT CTC 3'

LS203 (108-mer) (SEQ.ID.NO:99) 5' GCC CGC TCG CAG GGC CGA GCC CCA GCG CCA CAC CAT GCT GTG CAT GTG CTG CAA GTG CGA GGC CCG CAT CGA GCT GGT GGT GGA GAG CAG CGC TGA CGA CCT GCG CGC 3'

LS204 (109-mer) (SEQ.ID.NO:100) 5' CAG TCA GAT CTA GAG ATA TCT TTA CTG CTG GCT GGC GCA CCA GGG GCA CAC GAA GCT CAG GGT GTT CAG GAA CAG CTG CTG GAA GGC GCG CAG GTC GTC AGC GCT GCT C 3'

B. PCR Amplification Primers

LS205 (26-mer) (SEQ.ID.NO:101) 5' GTC ACA GAT CTG ATA TCG AAT TCC AC 3'

LS206 (27-mer) (SEQ.ID.NO:102) 5' CAG TCA GAT CTA GAG ATA TCT TTA CTG 3'

**FIG.22**

## Oligonucleotides used in the construction of HPV6 E2

6A 1-84 (90mer) (SEQ.ID.NO:103) 5' GAA TTC AGA TCT GAT ATC ACC ATG GAG GCC ATC GCC AAG CGC CTG GAC GCC TGC CAG GAG CAG CTG CTG GAG CTG TAC GAG GAG AAC AGC 3'

6B 65-157 (92mer) (SEQ.ID.NO:104) 5' CCT TGT ACA GCA GCA CGC TCT CGT GGC GCA TGC ACT TCC AGT GCA GCA CGT GCT TGT GCA GGT CGG TGC TGT TCT CCT CGT ACA GCT CCA GC 3'

6C 132-227 (96mer) (SEQ.ID.NO:105) 5' CCA CGA GAG CGT GCT GCT GTA CAA GGC CAA GCA GAT GGG CCT GAG CCA CAT CGG CAT GCA GGT GGT GCC TCC TCT GAA GGT GAG CGA GGC CAA GGG 3'

6D 202-304 (103mer) (SEQ.ID.NO:106) 5' GCA GGG TCC AGG GCT CCA TGC TGT ACT CGG TGC GCA GCA GGC TCT CGA GGT GCA TCT GCA TCT CGA TGG CGT TGT GGC CCT TGG CCT CGC TCA CCT TCA GAG G 3'

6E 276-373 (98mer) (SEQ.ID.NO:107) 5' CGA GTA CAG CAT GGA GCC CTG GAC CCT GCA GGA GAC CAG CTA CGA GAT GTG GCA GAC CCC TCC CAA GCG CTG CTT CAA GAA GCG CGG CAA GAC CGT GG 3'

6F 347-448 (102mer) (SEQ.ID.NO:108) 5' CGT TGT CCT GCA CGT ACA CGT CGG TCC ACA CCA CGT AGT CCA TGG TGT TGG CGC AGC CGT CGA ACT TCA CCT CCA CGG TCT TGC CGC GCT TCT TGA AGC 3'

6G 425-526 (102mer) (SEQ.ID.NO:109) 5' CCG ACG TGT ACG TGC AGG ACA ACG ACA CCT GGG TGA AGG TGC ACA GCA TGG TGG ACG CCA AGG GCA TCT ACT ACA CCT GTG GCC AGT TCA AGA CCT ACT ACG 3'

6H 495-586 (92mer) (SEQ.ID.NO:110) 5' GCT GCC GTA GCA CAC CTC CCA GTG CTT GGT GCT GCC GTA CTT CTC GGC CTC CTT CAC GAA GTT CAC GTA GTA GGT CTT GAA CTG GCC ACA GG 3'

6I 500-591 (94mer) (SEQ.ID.NO:111) 5' GCA CTG GGA GGT GTG CTA CGG CAG CAC CGT GAT CTG CAG CCC CGC TAG CGT GAG CAG CAC CAC CCA GGA GGT GAG CAT CCC CGA GAG CAC CAC C 3'

6J 636-732 (97mer) (SEQ.ID.NO:112) 5' GCG AGG AGG GGT CTG CAC GGC GTC CTC CTT GGT GCT GCT CAC CAG GGT GCT GGT CTG GGC GGG AGT GTA GGT GGT GCT CTC GGG GAT GCT CAC C 3'

FIG.23A

6K 708-804 (97mer) (SEQ.ID.NO:113) 5' GGA CGC CGT GCA GAC CCC TCC TCG CAA GCG CGC CCG CGG CGT GCA GCA GAG CCC CTG CAA CGC CCT GTG CGT GGC CCA CAT CGG CCC CGT GGA CAG C 3'

6L 780-873 (94mer) (SEQ.ID.NO:114) 5' GGC GCT GCT GTT GCT GTT GCG GCG CTG GTG CTG GTC GTG GTT GGT GAT CAG GTT GTG GTT GCC GCT GTC CAC GGG GCC GAT GTG GGC C 3'

6M 849-943 (95mer) (SEQ.ID.NO:115) 5' CCG CAA CAA CAG CAA CAG CAG CGC CAC TCC CAT CGT GCA GTT CCA GGG CGA GAG CAA CTG CCT GAA GTG CTT CCG CTA CCG CCT GAA CGA TCG CC 3'

6N 917-1012 (96mer) (SEQ.ID.NO:116) 5' CGT GCT TGT GGG GAG CCT TGC TGC TGG CCC AGT GCC AGG TGC TGC TGA TCA GGT CGA ACA GGT GGC GGT GGC GAT CGT TCA GGC GGT AGC GGA AGC 3'

6O 989-1083 (95mer) (SEQ.ID.NO:117) 5' GCA GCA AGG CTC CCC ACA AGC ACG CCA TCG TGA CCG TGA CCT ACG ACA GCG AGG AGC AGC GCC AGC AGT TCC TGG ACG TGG TGA AGA TCC CTC CC 3'

6P 1059-1154 (96mer) (SEQ.ID.NO:118) 5' CTC GAG AGA TCT CCC GGG TCT AGA GCT TAC AGC AGG TGC AGG CTC ATG AAG CCC AGC TTG TGG CTG ATG GTG GGA GGG ATC TTC ACC ACG TCC AGG 3'

6PA 25mer (SEQ.ID.NO:119) 5' GAA TTC AGA TCT GAT ATC ACC ATG G 3'

6PD 21mer (SEQ.ID.NO:120) 5' GCA GGG TCC AGG GCT CCA TGC 3'

6PE 25mer (SEQ.ID.NO:121) 5' CGA GTA CAG CAT GGA GCC CTG GAC C 3'

6PH 25mer (SEQ.ID.NO:122) 5' GCT GCC GTA GCA CAC CTC CCA GTG C 3'

6PI 21mer (SEQ.ID.NO:123) 5' GCA CTG GGA GGT GTG CTA CGG 3'

6PL 23mer (SEQ.ID.NO:124) 5' GGC GCT GCT GTT GCT GTT GC 3'

6PM 22mer (SEQ.ID.NO:125) 5' CCG CAA CAA CAG CAA CAG CAG C 3'

6PP 26mer (SEQ.ID.NO:126) 5' CTC GAG AGA TCT CCC GGG TCT AGA GC 3'

27/28

Oligonucleotides used to construct HPV18 E2

18A 1-97 (97mer) (SEQ.ID.NO:127) 5' GAA TTC AGA TCT GAT ATC ACC ATG CAG ACT CCC AAG GAG ACC CTG AGC GAG CGC CTG AGC GCC CTG CAG GA CAA GAT CAT CGA CCA CTA CGA GAA CG 3'

18B 69-166 (98mer) (SEQ.ID.NO:128) 5' CGA AGA AGA TGG CGT TCT CCC AGC GGA TCA GCT GCC AGT ACT GGA TCT GGC TGT CGA TGT CCT TGC TGT CGT TCT CGT AGT GGT CGA TGA TCT TGT CC 3'

18C 141-234 (94mer) (SEQ.ID.NO:129) 5' CCG CTG GGA GAA CGC CAT CTT CTT CGC CGC TCG CGA GCA CGG GAT CCA GAC CCT GAA CCA CCA GGT GGT GCC CGC CTA CAA CAT CAG CAA GAG C 3'

18D 211-304 (94mer) (SEQ.ID.NO:130) 5' CCT CGG TCT TGT AGG CGC TCT GGG CCA GGC CCT GCA GGG CCA TCT GCA GCT CGA TGG CCT TGT GGG CCT TGC TCT TGC TGA TGT TGT AGG CGG G 3'

18E 281-371 (91mer) (SEQ.ID.NO:131) 5' CCC AGA GCG CCT ACA AGA CCG AGG ACT GGA CCC TGC AGG ACA CCT GCG AGG AGC TGT GGA ACA CCG AGC CCA CCC ACT GCT TCA AGA AGG G 3'

18F 348-441 (94mer) (SEQ.ID.NO:132) 5' GCT GTC CCA GGC CAC GTA GTT CAT GCA GTT GTC CTT GTT GCC GTC GAA GTA CAC CTG CAC GGT CTG GCC TCC CTT CTT GAA GCA GTG GGT GGG C 3'

18G 416-505 (90mer) (SEQ.ID.NO:133) 5' GCA TGA ACT ACG TGG CCT GGG ACA GCG TGT ACT ACA TGA CCG ACG CCG GCA CCT GGG ACA AGA CCG CCA CCT GCG TGA GCC ACC GCG GCC 3'

18H 481-572 (92mer) (SEQ.ID.NO:134) 5' CCG TAC TTC TCG CAC TCG CTC TTG AAC TCG ATG TAG AAG GTG TTG TAG CCC TCC TTC ACG TAG TAC AGG CCG CGG TGG CTC ACG CAG GTG GC 3'

18I 543-636 (94mer) (SEQ.ID.NO:135) 5' CGA GTT CAA GAG CGA GTG CGA GAA GTA CGG CAA CAC CGG CAC CTG GGA GGT GCA CTT CGG CAA CAA CGT GAT CGA CTG CAA CGA CAG CAT GTG C 3'

18J 609-708 (100mer) (SEQ.ID.NO:136) 5' GCT GTA GGG GCT GGG AGT GTG CTG CAG CTG CTT CAC CAG CTG GGT GGC GCT CAC GGT GTC GTC GCT GGT GCT GCA CAT GCT GTC GTT GCA GTC GAT CAC G 3'

FIG.24A

18K 687-779 (93mer) (SEQ.ID.NO:137) 5' GCA CAC TCC CAG CCC CTA CAG CAG CAC CGT GAG CGT GGG CAC CGC CAA GAC CTA CGG CCA GAC CAG CGC CGC CAC TCG CCC TGG CCA CTG CGG 3'

18L 758-853 (96mer) (SEQ.ID.NO:138) 5' GCT TGT TGT TGC CGG TGG CGG CGG CGC CCA GCA GAG GGT TCA CGG GCC CGC AGT GCT GCT TCT CGG CCA GGC CGC AGT GGC CAG GGC GAG TGG 3'

18M 829-925 (97mer) (SEQ.ID.NO:139) 5' GCC ACC GCC ACC GGC AAC AAC AAG CGC CGC AAG CTG TGC AGC GGC AAC ACC ACT CCC ATC ATC CAC CTG AAG GGC GAC CGC AAC AGC CTG AAG TGC C 3'

18N 900-996 (97mer) (SEQ.ID.NO:140) 5' GGC GCC GGT CCA GTG CCA GGT GCT GCT GAT GTC GCG GTA GTG GTC GCT GTG CTT GCG CAG GCG GTA CCG CAG GCA CTT CAG GCT GTT GCG GTC GCC C 3'

18O 974-1072 (99mer) (SEQ.ID.NO:141) 5' GCA CCT GGC ACT GGA CCG GCG CCG GGA ACG AGA AGA CCG GCA TCC TGA CCG TGA CCT ACC ACA GCG AGA CCC AGC GCA CCA AGT TCC TGA ACA CCG TGG 3'

18P 1048-1145 (98mer) (SEQ.ID.NO:142) 5' CTC GAG AGA TCT CCC GGG TCT AGA GCT TAC ATG GTC ATG TAG CCC ACC AGG ATC TGC ACG CTG TCG GGG ATG GCC ACG GTG TTC AGG AAC TTG GTG CG 3'

18PA 25mer (SEQ.ID.NO:143) 5' GAA TTC AGA TCT GAT ATC ACC ATG C 3'

18PD 23mer (SEQ.ID.NO:144) 5' CCT CGG TCT TGT AGG CGC TCT GG 3'

18PE 21mer (SEQ.ID.NO:145) 5' CCC AGA GCG CCT ACA AGA CCG 3'

18PH 21mer (SEQ.ID.NO:146) 5' CCG TAC TTC TCG CAC TCG CTC 3'

18PI 20mer (SEQ.ID.NO:147) 5' CGA GTT CAA GAG CGA GTG CG 3'

18PL 21mer (SEQ.ID.NO:148) 5' GCT TGT TGT TGC CGG TGG CGG 3'

18PM 25mer (SEQ.ID.NO:149) 5' GCC ACC GCC ACC GGC AAC AAC AAG C 3'

18PP 26mer (SEQ.ID.NO:150) 5' CTC GAG AGA TCT CCC GGG TCT AGA GC 3'

**FIG.24B**